

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 20 Seconds
(without alignments)
48.108 Million cell updates/sec

Title: US-10-083-768-5

Perfect score: 25

Sequence: 1 XXGXXXXXXW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	68.0	72	2	H90603
2	17	68.0	132	2	C41855
3	17	68.0	165	2	A83349
4	17	68.0	203	2	T50044
5	17	68.0	239	2	T37065
6	17	68.0	251	2	A84019
7	17	68.0	272	2	T15820
8	17	68.0	297	2	E96002
9	17	68.0	308	2	B84311
10	17	68.0	406	2	A47696
11	17	68.0	408	2	D70549
12	17	68.0	408	2	H87193
13	17	68.0	433	2	C59222
14	17	68.0	492	2	T39591
15	17	68.0	523	2	T36677
16	17	68.0	547	2	A95861
17	17	68.0	579	2	T35240
18	17	68.0	624	2	S74222
19	17	68.0	735	2	AC0858
20	17	68.0	776	1	JQ2022
21	17	68.0	776	1	JQ2023
22	17	68.0	776	1	VEXRBU
23	17	68.0	776	1	VEXRBU
24	17	68.0	776	1	VEXRBU
25	17	68.0	776	1	VEXRBU
26	17	68.0	776	1	VEXRBU
27	17	68.0	776	1	VEXRBU
28	17	68.0	776	2	A48480
29	17	68.0	776	2	S03611

30	17	68.0	823	2	T02812
31	17	68.0	870	2	AB0570
32	17	68.0	1029	2	F96602
33	17	68.0	1156	2	S19306
34	17	68.0	1275	1	S53636
35	17	68.0	1546	2	G90603
36	17	68.0	1596	2	AG2501
37	17	68.0	1680	1	C5MS
38	17	68.0	2062	2	G96602
39	17	68.0	2204	1	RRNZNV
40	17	68.0	4563	1	LPHUB
41	17	68.0	4660	2	T42737
42	16	64.0	12	2	FQ0776
43	16	64.0	60	2	AC2981
44	16	64.0	65	2	T35419
45	16	64.0	70	2	A30518

ALIGNMENTS

RESULT 1

H90603

hypothetical protein MYPV_7360 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90603

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: H90603

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-72 <CUR>

A:Cross-references: UNIPROT:Q98PI6; GB:AL445566; PID:gl4090151; PIDN:CAC13909.1; GSPDB:G

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV_7360

A:Genetic code: SGC3

Query Match 68.0%; Score 17; DB 2; Length 72;
Best Local Similarity 28.6%; Pred. No. 8.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	3	GXXXXXW	9
Db	39	GAATSW	45

RESULT 2

C41855

hypothetical 14.2K beta-lactamase regulatory protein - Streptomyces cacaoi
C:Species: Streptomyces cacaoi

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: C41855

R:Urabe, H.; Ogawara, H.

J. Bacteriol. 174, 2834-2842, 1992

A:Title: Nucleotide sequence and transcriptional analysis of activator-regulator protein:

A:Reference number: A41855; MUID:92234939; PMID:1569015

A:Accession: C41855

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <URA>

A:Cross-references: UNIPROT:P33654; GB:P00937; NID:g216997; PIDN:BAA00776.1; PID:g217001

A>Note: sequence extracted from NCBI backbone (NCBIN:97018, NCBIIP:97029)

C:Superfamily: Streptomyces cacaoi hypothetical 14.2K beta-lactamase regulatory protein

Query Match 68.0%; Score 17; DB 2; Length 132;
Best Local Similarity 28.6%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	3	GXXXXXW	9
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Db      53 GSSASSW 59

RESULT 3
A83349
hypothetical protein PA2367 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <STO>
A;Cross-references: UNIPROT:Q911B2; GB:AE004663; GB:AE004091; NID:g9948405; PIDN:AAG0575
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2367

Query Match      68.0%; Score 17; DB 2; Length 165;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      150 GTAAATW 156

RESULT 4
T50044
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Haloarcula marismortui
C;Species: Haloarcula marismortui
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50044
R;Joshi, P.B.; Dennis, P.F.
J. Bacteriol. 175, 1561-1571, 1993
A;Title: Characterization of paralogous and orthologous members of the superoxide dismut
A;Reference number: Z25029; MUID:93194779; PMID:8449865
A;Accession: T50044
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-203 <JOS>
A;Cross-references: UNIPROT:Q03302; EMBL:M97485; NID:gi148741; PIDN:AAV73374.1; PID:gi1487
C;Genetics:
A;Gene: sod
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase

Query Match      68.0%; Score 17; DB 2; Length 203;
Best Local Similarity 28.6%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      60 GSSAAAW 66

RESULT 5
T37065
hypothetical protein SCJ21.16 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37065
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21620
A;Accession: T37065

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-272 <MAR>
A;Cross-references: UNIPROT:Q18776; EMBL:U41276; NID:gi1086884; PID:gi1086886; PIDN:AAA8246
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C52B11.2
A;Introns: 12/1; 91/3; 190/3; 221/3

Query Match      68.0%; Score 17; DB 2; Length 272;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      77 GSSSSSW 83

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-239 <SEE>
A;Cross-references: UNIPROT:Q9S1Z1; EMBL:AL109747; PIDN:CAB52362.1; GSPDB:GN00070; SCOREDI
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ21.16

Query Match      68.0%; Score 17; DB 2; Length 239;
Best Local Similarity 28.6%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      172 GASAAAW 178

RESULT 6
A84019
NADPH-flavin oxidoreductase BH2953 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84019
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84019
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <STO>
A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; GB:BA000004; NID:gi10175500; PIDN:BA8066;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2953
C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match      68.0%; Score 17; DB 2; Length 251;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      211 GATTTTW 217

RESULT 7
T15820
hypothetical protein C52B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15820
R;Martin, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C52B11.
A;Reference number: Z18411
A;Accession: T15820
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-272 <MAR>
A;Cross-references: UNIPROT:Q18776; EMBL:U41276; NID:gi1086884; PID:gi1086886; PIDN:AAA8246
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C52B11.2
A;Introns: 12/1; 91/3; 190/3; 221/3

Query Match      68.0%; Score 17; DB 2; Length 272;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      77 GSSSSSW 83

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RESULT 8
E96002
Probable sugar uptake ABC transporter permease protein SMB21459 [imported] - Sinorhizobium
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: E96002
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11461431
A:Accession: E96002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KUR>
A:Cross-references: UNIPROT:Q92U54; GB:AL591985; PIDN:CAC49685.1; PID:g15141172; GSPDB:C
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB21459
A:Genome: plasmid
C:Superfamily: inner membrane protein ugpA

Query Match 68.0%; Score 17; DB 2; Length 297;
Best Local Similarity 28.6%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 268 GAAASTW 274

RESULT 9
B84311
Hypothetical protein Vng1578h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84311
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: UNIPROT:Q9HPL3; GB:AE004437; NID:g10581062; PIDN:AAG19854.1; GSPDB:C
C:Genetics:
A:Gene: VNG1578H
C:Superfamily: cobalamin biosynthesis protein D

Query Match 68.0%; Score 17; DB 2; Length 308;
Best Local Similarity 28.6%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 172 GAAAAAW 178

RESULT 10

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A47696
Acetamidase - Mycobacterium smegmatis
C:Species: Mycobacterium smegmatis
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47696
R:Manenthiralingam, E.; Draper, P.; Davis, E.O.; Colston, M.J.
J. Gen. Microbiol. 139, 575-583, 1993
A:Title: Cloning and sequencing of the gene which encodes the highly inducible acetamida
A:Reference number: A47696; MUID:93232774; PMID:8473863
A:Contents: NCTC 8159
A:Accession: A47696
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-406 <MAH>
A:Cross-references: UNIPROT:Q07838; GB:X57175; GB:S59037; NID:g312080; PIDN:CAA40462.1;
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:129965, NCBIP:129966)

Query Match 68.0%; Score 17; DB 2; Length 406;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 370 GASAAASW 376

RESULT 11
D70549
Hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70549
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70549
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <COL>
A:Cross-references: UNIPROT:O06427; GB:Z95558; GB:AL123456; NID:g3261781; PIDN:CAB08972.
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0561c
C:Superfamily: fixC protein

Query Match 68.0%; Score 17; DB 2; Length 408;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 18 GSAAAAW 24

RESULT 12
H87193
Probable FAD-linked oxidoreductase ML2276 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87193
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87193

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9CBA6; GB:AL450380; NID:g13093912; PIDN:CAC31792.1; GSPDB:G
C;Genetics:
A;Gene: ML2276

Query Match 68.0%; Score 17; DB 2; Length 408;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 18 GSAAATW 24

RESULT 13

C69222
hypothetical protein MTH913 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69222
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69222
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-433 <MTH>
A;Cross-references: UNIPROT:Q26998; GB:AE000066; NID:g2622009; PIDN:AAB8541
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH913
A;Start codon: GTG

Query Match 68.0%; Score 17; DB 2; Length 433;
Best Local Similarity 28.6%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 391 GSASSW 397

RESULT 14

I39591
hemolysin - Aeromonas hydrophila
N;Alternate names: aerolysin
C;Species: Aeromonas hydrophila
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39591; I39590; S26573; S26574
R;Hirono, I.; Aoki, T.; Asao, T.; Kozaki, S.
Microb. Pathog. 13, 433-446, 1992
A;Title: Nucleotide sequences and characterization of haemolysin genes from Aeromonas hy
A;Reference number: I39590; MUID:93254202; PMID:1302284
A;Accession: I39591
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-492 <RES>
A;Cross-references: UNIPROT:Q06303; EMBL:X65043; NID:g38816; PIDN:CAA46179.1; PID:g38817
A;Accession: I39590
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-56, 'V', 58-295, 'P', 297-492 <RES2>
A;Cross-references: EMBL:X65044; NID:g38814; PIDN:CAA46180.1; PID:g38815
A;Experimental source: strain 28SA
C;Superfamily: aerolysin

Query Match 68.0%; Score 17; DB 2; Length 492;
Best Local Similarity 28.6%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GXXXXXXW 9
Db 91 GSASSTW 97

RESULT 15

T36677
probable secretory protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36677
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21611
A;Accession: T36677
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-523 <SEE>
A;Cross-references: UNIPROT:Q9X921; EMBL:AL035636; PIDN:CAB38493.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE08:SCH5.19c

Query Match 68.0%; Score 17; DB 2; Length 523;
Best Local Similarity 28.6%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 85 GSATTTW 91

Search completed: January 31, 2005, 18:22:34
Job time : 21 secs